

APPROVED	BY
CLASS	SUBCLASS
DRAFTSMAN	

**BLASTP ALIGNMENT OF SEQ ID NO: 4 METALLOCARBOXYPEPTIDASE-LIKE POLYPEPTIDE
WITH BOTHROPS JARARACA CARBOXYPEPTIDASE HOMOLOG SEQ ID NO: 20**

Score: 826 (295.8 bits), Expect = 3.2e-82, P = 3.2e-82
 Identities = 152 / 326 (46%), Positives = 219 / 326 (67%)
 Subject: >gb|AAF01344.1| (AF190274) carboxypeptidase homolog [Bothrops jararaca] (SEQ ID NO: 20)
 Length = 416

Score = 826 (295.8 bits), Expect = 3.2e-82, P = 3.2e-82
 Identities = 152 / 326 (46%), Positives = 219 / 326 (67%)

Query:	13	MLVPGGLGYDRSLAQHROEITVDKSVPWSLET-YSYNTIYHPMGEIYEWREISEKYKEVV	71
	+L	GL Y+ L + Q ++D+ + +	+ I W + I + + +V
Sbjct:	82	LLQSGLNYE-ILLDNLQAVLDRQLDNHARTAGNYEKYNSWEKIDAWTADIANENPSLV	140
Query:	72	TQHFLGVTYETHPIYYLKLISOPPSGNPKKKIIMMDCGIHAREWIAPAFQCQWFWKEILQNHKD	131
	++ +G T+E P+	LK+ +P N KK I++DCG HAREWI+PAFCQWFW+E ++ +	
Sbjct:	141	SRLQIGTTFEGRPMPLLKVGKPGVN-KKAIFIDCGFIAHREWISPAFCQWFWREAVRTYKG	199
Query:	132	NSRIRKLRLNLDFYVLPVLNIDGYIYTWTTDRLWRKRSRSPHNNGTCFGTDLNRFNFSWC	191
	++ + LL LDFY+LPVLNIDGY+Y+W	R+WRK+RS + TC GTD NRNF+A+WC	
Sbjct:	200	ETIMTQLLNKLDFYVLPVLNIDGYVYSWKQSRRMWRKTRSVNAGSTCIGTDPNRNFDAAWC	259
Query:	192	SIGASRNQCDQTFCGTGPVSEPETKAVASFIESRKDDILCFCLTHMSYGQLILTPGYTKN	251
	S+GASRN +T+CG+ P SE ETKA+A FI + I +LT+HSY Q+L PY YT +		
Sbjct:	260	SVGASRNPCSETYCGSKPESEKETKALADFIRRNRSSIIQAYLTHSYSQMLLYPYSYTYD	319
Query:	252	KSSNHPEMIQVGQKAANALKAKYGTNYRVGSSADILYASSGSSRDWARDIGIPFSYTFEL	311
	+SN+ ++ + +A LK +GT Y G A +Y ++G S DWA D GI +++TFEL		
Sbjct:	320	LTSNNKKLNLSIAKEAIRELKVLFGTEYTYGPQAATIYPAAGGSSDDWAYDQQGIKYAFTFEL	379
Query:	312	RDSGTGTVLPEAQIQOPTCEETMEAV	337
	RD G YGF LPE+QI+PTCEETM AV		
Sbjct:	380	RDKGRYGFALPESQIKPCTCEETMIAV	405

FIG: 1

APPROVED BY	O.G. FIG.
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BLASTP ALIGNMENT OF SEQ ID NO: 4 METALLOCARBOXYPEPTIDASE-LIKE POLYPEPTIDE WITH HUMAN CARBOXYPEPTIDASE B MUTANT (G251N, D253R) -HCPB-(HIS) 6-C-MYC SEQ ID NO: 21

Query: Carboxypeptidase-like protein (SEQ ID 4)
 Subject: >sp|W13751|W13751 Carboxypeptidase B mutant (G251N,D253R) -HCPB-(His) 6-c-myc (SEQ ID NO: 21)
 Length = 349

Score = 811 (290.5 bits), Expect = 6.2e-81, P = 6.2e-81
 Identities = 150/312 (48%), Positives = 206/312 (66%)

Query: 45 YSYNTIYHPMGEIYEWMMREIYESEKYYKEVYVTQHFLGVTYETHPIYYLKISQPSGNPKKIIWMD 104
 +SY Y+ I W +++++ + +++ + G T+E IY LK+ + +G K I+MD
 Sbjct: 26 HSYEKYNKWKETIEAWTQQVATENPALIISRSGVIGTTFEGRAYIYLKVKG-AQONKPAIFMD 84

Query: 105 CGIHAREWIAPAFCQCWFVKEILQLNHKDNRKLLRNLDFYVLPVLNIDGYIYTWTIDRL 164
 CG HAREWI+PAFCQCWFV+E + + + + +LL LDFYVLPVLNIDGYIYTWT
 Sbjct: 85 CGFHAREWISPAFCQCWFVREAVRTYGREIYQVTELLDKLDFYVLPVLNIDGYIYTWTKSRF 144

Query: 165 WRKSRSRPHNNGTCTGGDLNRFNFSWC SIGASRNCQDDQTFCGTPVSEPETKAVASFILES 224
 WRK+RS H +C GTD NRNF+A WC IGASRN D+T+CG SE ETKA+A FI +
 Sbjct: 145 WRKTRSTHTGSSCITGDPNRFNDAGWCEIGASRNPCDETYCPAAESEKETKALADFIRN 204

Query: 225 KRDDILCFLTMHSYGQLILTPYGYTKNKSSNHNPEMIQVGQKAANALAKAYGNTNYRGSSA 284
 K I +LT+HSY Q++ PY Y N+ E+ + + L + +GT Y G A
 Sbjct: 205 KLSSIKAYLTIHSYSQMMIYPYSAYKLGENNAELNALAKATVKELASLHGTYGPGGA 264

Query: 285 DILYASSGSSRDWARDIGIPESYTFELRDSGTYGFVLPFAQIQPTCEETMEA---VLS-V 340
 +Y ++G+SRDWA D GI +S+TFELRD+G YGF+LPE+QI+ TCEET A V S V
 Sbjct: 265 TTIYPAAAGNSRDAYDQGIRYSFTFELRTGRYGLLPESQIRATEETFLAIKYVASYV 324

Query: 341 LDDVYAKHWHD 352
 L+ +Y H H +
 Sbjct: 325 LEHLYHHHHHE 336

FIG. 2